SEQUENCE LISTING

<110>   Sakowicz, Roman
        Goldstein, Lawrence

<120>   Identification and Expression of Novel Kinesin Motor Protein

<130>   UCSD-04871

<140>   09/724,586
<141>   2000-11-28

<160>   9

<170>   PatentIn version 3.2

<210>   1
<211>   784
<212>   PRT
<213>   Thermomyces lanuginosus

<220>
<221>   MISC_FEATURE
<223>   TL-gamma ATP-dependent plus end-directed microtubule motor
        protein

<220>
<221>   DOMAIN
<222>   (1)..(357)
<223>   kinesin-like microtubule motor domain

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<221>   DOMAIN
<222>   (358)..(442)
<223>   neck domain links motor domain to stalk domain

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<222>   (602)..(784)
<223>   tail domain

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Gly Asn Gln Thr Ile Leu Thr Pro Pro Pro Gly Ala Glu Glu Lys Ala
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Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe
    50   55   60

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Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg
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Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala
                85              90              95

Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser
            100             105             110

Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile
        115             120             125

Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys
    130             135             140

Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr
145             150             155             160

Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu
            165             170             175

Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala
            180             185             190

Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu
            195             200             205

Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser
    210             215             220

Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His
225             230             235             240

Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu
            245             250             255

Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly
            260             265             270

Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu
            275             280             285

Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys
    290             295             300

Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
305             310             315             320
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Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile
              325                 330                 335

Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr
              340                 345                 350

Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp
              355                 360                 365

Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu
    370                 375                 380

Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Gly
385                 390                 395                 400

Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu
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Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
              420                 425                 430

Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
    435                 440                 445

Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
    450                 455                 460

Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile
465                 470                 475                 480

Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
              485                 490                 495

Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
              500                 505                 510

Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
              515                 520                 525

Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
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Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
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Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
             565             570             575

Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
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His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
             595             600             605

His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
    610             615             620

Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
625             630             635             640

Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
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Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
        660             665             670

Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
        675             680             685

Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
    690             695             700

Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
705             710             715             720

Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
             725             730             735

Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
             740             745             750

Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln
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Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe
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cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag   180
gcatttgcgt tcgatcggtc gtattggtcc tttgacaaga atgctcccaa ctatgcgaga   240
caggaagacc tattccaaga tatcggagtc ccgcttctgg ataatgcatt caagggttat   300
aacaattgta tcttcgccta cggtcagacc ggttcgggca agtcctattc aatgatgggc   360
tatggcaagg agcatggcgt gatcccgcgg atttgccagg acatgttccg gcgtattaat   420
gaactgcaga aggacaagaa cctcacttgc aacgtcgaag tttcgtactt ggaaatttac   480
aatgaacgag tgcgagactt gctgaatccg tcgacaaagg ggaatctcaa ggtccgagaa   540
cacccgtcga ccggcccta cgtggaggac ttggcgaagc tggtcgtgcg atcattccaa   600
gaaatcgaaa atctcatgga tgagggcaac aaagccagaa cggttgccgc cacaaacatg   660
aacgagacat ccagtcgatc ccacgccgtc ttcactttga ccttgacgca aaagtggcat   720
gatgaagaga ccaaaatgga cacagagaag gttgcgaaga tcagtctggt agatttggcg   780
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ggaaaacaga agaagaatca gttagtacct taccgagatt cggtactgac gtggcttctg   960
aaggactcct tgggaggcaa ctcgatgacc gccatgattg ccgccatttc gcctgctgat  1020
attaactttg aagagactct cagtacccctt cgatatgcgg actctgcgaa gcgaatcaag  1080
aaccacgcag tggtcaatga agacccgaac gcgcggatga tccgcgagtt gaaggaggaa  1140
ctcgcgcagc tgaggagcaa actccagagc agtggtggag gtggaggtgg tgcaggaggt  1200
tctggcgggc cagtggagga atcgtacccg cccgacacgc cgctcgagaa gcaaatcgtg  1260
tcgattcagc agcaggatgc gacagtcaag aaaatgagca aggcagaaat cgtggagcaa  1320
ctgaaccaga gtgagaagct ctatcgggat ctcaatcaga cctgggaaga gaagctggcc  1380
aagaacgagg aaatccacaa ggaacgagaa gcggcgctcg aggagctggg tatcagcatc  1440
gaaaagggct ttgttggccc ttaccactcc aaagaaatgc acatctagt caacttgagc  1500
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gaacactgta cgtttgaaaa tgtggacaac gttgtgacca tcgtgccaaa cgagaaggct   1680

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atcatcctgg gcgatttcca cattttttcga ttcaaccatc cggaagaagc tcgtgcggaa   1800

cggcaagaac aatccttgct tcgccattct gtcaccaaca gtcagttggg ttcgcctgct   1860

ccaggccgtc acgaccggac actgagcaag gcgggttcgg atgcggacgg cgattctcgc   1920

tcagattctc ctttgccgca ctttcgtgga aaggatagcg actggttcta tgctcgcagg   1980

gaagctgcta gcgcgatcct agggttggat cagaagatct ctcatctgac agatgacgag   2040

ttggatgcat tatttgacga tgttcagaaa gcgcgggcag ttcgtcgtgg gctggtcgaa   2100

gacaacgaag atagcgattc gcagagttcg tttccggtcc gtgacaaata catgtccaat   2160

ggaaccattg ataatttctc gctcgatacc gccattacta tgccgggtac ccctcgtagt   2220

gatgacgacg gtgacgcgct gtttttttggt gataagaagt cgaaacagga tgcgtctaat   2280

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aagcaggaat tc                                                       2352


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<220>
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